

FIG. 1

HSP 90-beta (Mouse)
SEQ ID NO:1

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1 mpeevvhgee evetfafgae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpskldsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkhsqfig ypitlyleke rekeisddea eeekgekeee
241 dkddeekpki edvgsdeedd sgdkkkkktk kikekyidqe elnktkpiwt rnpdditqee
301 ygefysltn dwedhlavkh fsvegglefr allfiprrap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremllqski lkvirknivk kclelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketg
481 ksiyyitges keqvansafv ervrkrgefv vymtepiday cvqqlkefdg kslvsvtkeg
541 lelpedeeek kkmeeskakf enlcklmkei ldckvekti snrlvsspc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeadkndka vkdlvllfe
661 tallssgfsl edpqthsnri yrmiklglgi dedevaaep naavpdeipp legdedasrm
721 eevd

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HSP 90-beta (Human)
SEQ ID NO:2

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1 mpeevvhgee evetfafgae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpskldsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkhsqfig ypitlyleke rekeisddea eeekgekeee
241 dkddeekpki edvgsdeedd sgdkkkkktk kikekyidqe elnktkpiwt rnpdditqee
301 ygefysltn dwedhlavkh fsvegglefr allfiprrap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremllqski lkvirknivk kclelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketg
481 ksiyyitges keqvansafv ervrkrgefv vymtepiday cvqqlkefdg kslvsvtkeg
541 lelpedeeek kkmeeskakf enlcklmkei ldckvekti snrlvsspc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeadkndka vkdlvllfe
661 tallssgfsl edpqthsnri yrmiklglgi dedevaaep naavpdeipp legdedasrm
721 eevd

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HSP 90-alpha (Human)
SEQ ID NO:3

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1 mpeetqtqdq pmeeeevetf afgaeiaqlm sliintfysn keiflrelis nssdaldkir
61 yesltdpskl dsgkelhinl ipnkqdrtilt ivdtgigmtk adlinnlgti aksgtkafme
121 alqagadism igqfgvgfys aylvaekvtv itkhnnddeg awessaggsf tvrttdtgepm
181 grgtkvilhl kedqteylee rrikeivkhh sqfigypitl fvekerdkev sddeaeeked
241 keeekekeek esedkpeied vgsdeeeekk dgdkkkkkki kekyidqeel nktkpiwtrn
301 pdditneeyg efyksltn dwedhlavkhfs vegglefral lfvprrapfd lfenrkkknn
361 iklyvrrvfi mdnceelipe ylnfirgvvd sedlplnir emlqgskilk virknlvkcc
421 lelftelaed kenykkfyeg fskniklgih edsqrkkls ellryytsas gdemvslkdy
481 ctrmkenqkh iyyitgetkd qvansafver lrkhgleviy miepidaycv qqlkefegkt
541 lvsvtkegle lpedeeekkk geekktkfen lckimkdile kkvekvvsn rlvtsppciiv
601 tstygwtanm erimkaqalr dnstmgymaa kkhleinpdh siietlrqka eadkndksvk
661 dlillyeta llssgfsled pqthanriy miklglgide ddptaddtsa avteempple
721 gdddtzrmee vd

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HSP 84 (Mouse)
SEQ ID NO:4

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1 mpeevvhgee evetfafgae iaqlmsliin tfysnkeifl relisnasda ldkiyeslt
61 dpskldsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkhsqfig ypitlyleke rekeisddea eeekgekeee
241 dkedeeekpi edvgsdeedd sgdkdkkktk kikekyidqe elnktkpiwt rnpdditqee
301 ygefysltn dwedhlavkh fsveggflef allfiprrap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremllqgski lkvrknivk kclelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgefv vymtepiday cvqqlkefdg kslvsvtkeg
541 lelpedeeek kkmeeskakf enlcklmkei ldkkvekvti snrlvsspc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeadkndka vkdlvllfe
661 tallssgfsl edpqthsnri yrmiklglgi dedevtaeep saavpdeipp legdedasrm
721 eevd

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HSP 84 (Human)
SEQ ID NO:5

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1 mpeevvhgee evetfafgae iaqlmsliin tfysnkeifl relisnasda ldkiyeslt
61 dpskldsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkhsqfig ypitlyleke rekeisddea eeekgekeee
241 dkddeekpki edvgsdeedd sgdkdkkktk kikekyidqe elnktkpiwt rnpdditqee
301 ygefysltn dwedhlavkh fsveggflef allfiprrap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremllqgski lkvrknivk kclelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgefv vymtepiday cvqqlkefdg kslvsvtkeg
541 lelpedeeek kkmeeskakf enlcklmkei ldkkvekvti snrlvsspc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeadkndka vkdlvllfe
661 tallssgfsl edpqthsnri yrmiklglgi dedevaaeep naavpdeipp legdedasrm
721 eevd

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HSP 86 (Mouse)
SEQ ID NO:6

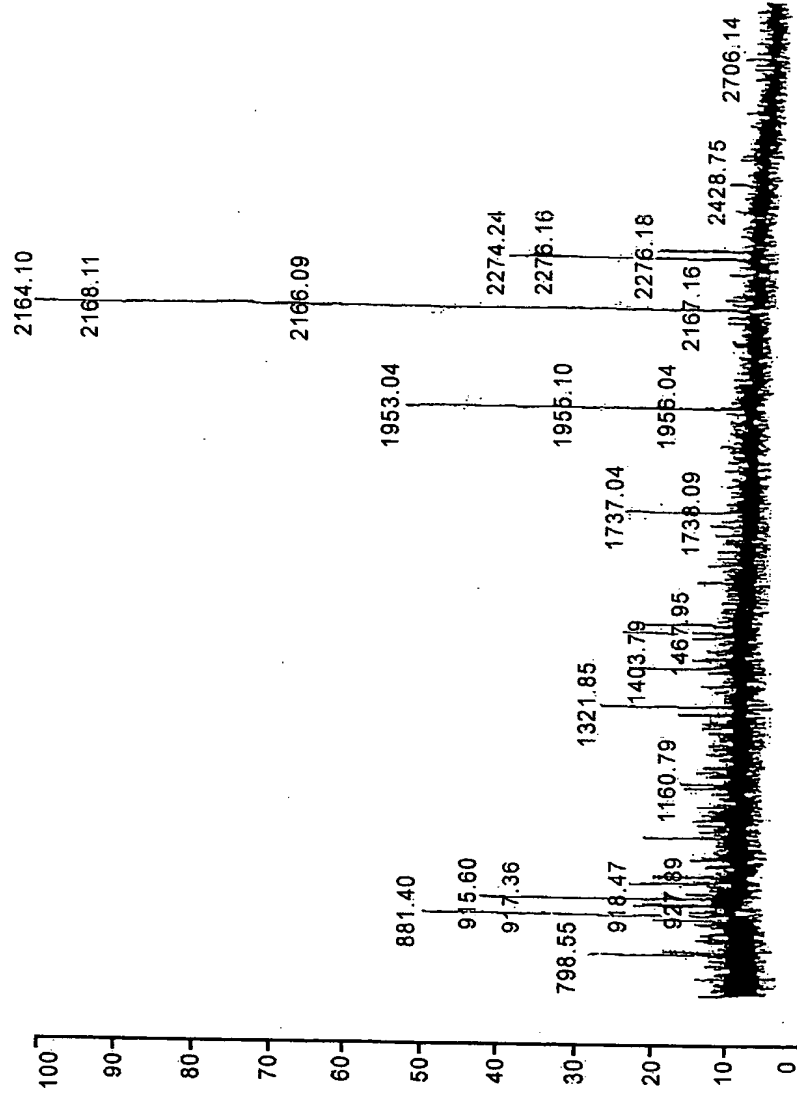
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1 mpeetqtqdg pmeeeevetf afgaeiaqlm sliintfysn keiflrelis nssdaldkir
61 yesltdpskl dsgkelhinl ipskqdrtl ivdtgigmtk adlinnlgti aksgkafme
121 alqagadism igqfgvgfys aylvaekvtv itkhnndegy awessaggsf tvrttdtgepm
181 grgtkvilhl kedqteylee rrikeivkhh sqfigypitl fvekerdkev sddeaeekke
241 keeekkeek esddkpeied vgsdeeeek kdgdkkkkkk ikeyidqee lnktkpiwtr
301 npdditneey gefyksltn dwedhlavkh fsveggflef llfvprrapf dlfenrkkkn
361 niklyvrrvf imdnceelip eynlfirgv dsedlplnis remllqgskil kvirknlvkk
421 clelftelae dkenykkfy qfsknklgi hedsqnrkkl sellryytsa sgdemvslkd
481 yctrmkcnqk hiyfitgetk dqvansafve rlrkhglevi ymiepiday cvqqlkefegk
541 tlsvstkegl elpedeeek kqeeektkfe nlckimkdil ekkvekvvvs nrlvtspcci
601 vtstygwtan merimkaqa lrdnstmgyma akkhleinpd hsiietlrq aeadkndksv
661 kdlvillyet allssgfsle dpqthanriy rmiklglgid eddptvddts aavteemopl
721 egddtsrme evd

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FIG. 10



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HSP 86, HSP 60 (Human)
SEQ ID NO:7

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1 mrlrlptvfrq mrpvsirvlap hltrayakdv kfgadaralm lqgvdllda vavtmgpkgr
61 tviieqswgs pkvtkdgvttv aksidlkdky knigaklvqd vanntneeag dgtttatvla
121 rsiakegfek iskganpvei rrgvmlavda viaelkkqsk pvttpееiaq vatisangdk
181 eigniidam kkvggrkgvit vkdgktlnde leiiegmkd rgyispyfin tskgqkcefq
241 dayvllsekk issiqsiyppa leianahrkp lviiadvdg ealstlvlnr lkvglqvav
301 kapgfgdnrk nqlkdmaiat ggavfgeegl tlnledvqph dlqkvgeviv tkddamlkg
361 kgdkaqiekr iqeiieqldv ttseyekekl nerlaklsdg vavlkvggts dvevnekkdr
421 vtdalnatra aveegivlgg gcallrcipa ldsltpaned qkigieiikr tlkipamtia
481 knagvegsli vekimqssse vgydamagdf vnmvekgiid ptkvvtall daagvasilt
541 taevvvteip keekdpngma mggmgggmgg gmf
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L-plastin (Human)
SEQ ID NO:8

```
1 margsvsdee mmelreafak vtdgngyis fnelndlfka acplpggyrv reitenlmat
61 gdldqdgri fdefikifhg lkstdvaktf rkainkkegi caiggtseqs svgtqhsyse
121 eekyafvnwi nkalendpdc rhvipmpnt ndlfnavgdg ivlckminls vpdtiderti
181 nkkltpfti qenlnlals asaigchvvn igaedlkegk pylvlglwq vikiglfadi
241 elsrnealia llregesled lmklspeell lrwanyhlen agcnkignfs tdikdskayy
301 hileqvapkg deegvpavvi dmsglrekdd iqraecmlqg aerlgcrqfv tatdvrgnp
361 klnlafianl fnrypalkhp enqdidwgal egetreertf rnwmmslgvn prvnhllysd
421 sdalvifgly ekikvpvdown rvnkppypkl ggnmkklenc nyavelgknq akfslvgigg
481 qdlnegnrtl tlaliwqlmr rytlnileei gggqkvnddi ivnwvnetlr eaeksssis
541 fkdpkistsl pvldlidaiq pgsinydllk tenlnddekl nnakyaisma rkigarvyal
601 pedlvevnpk mvmtvfacim gkgmkrv
```

FIG. 2
EL4 Conditioned Media Repels T cell *in vitro*

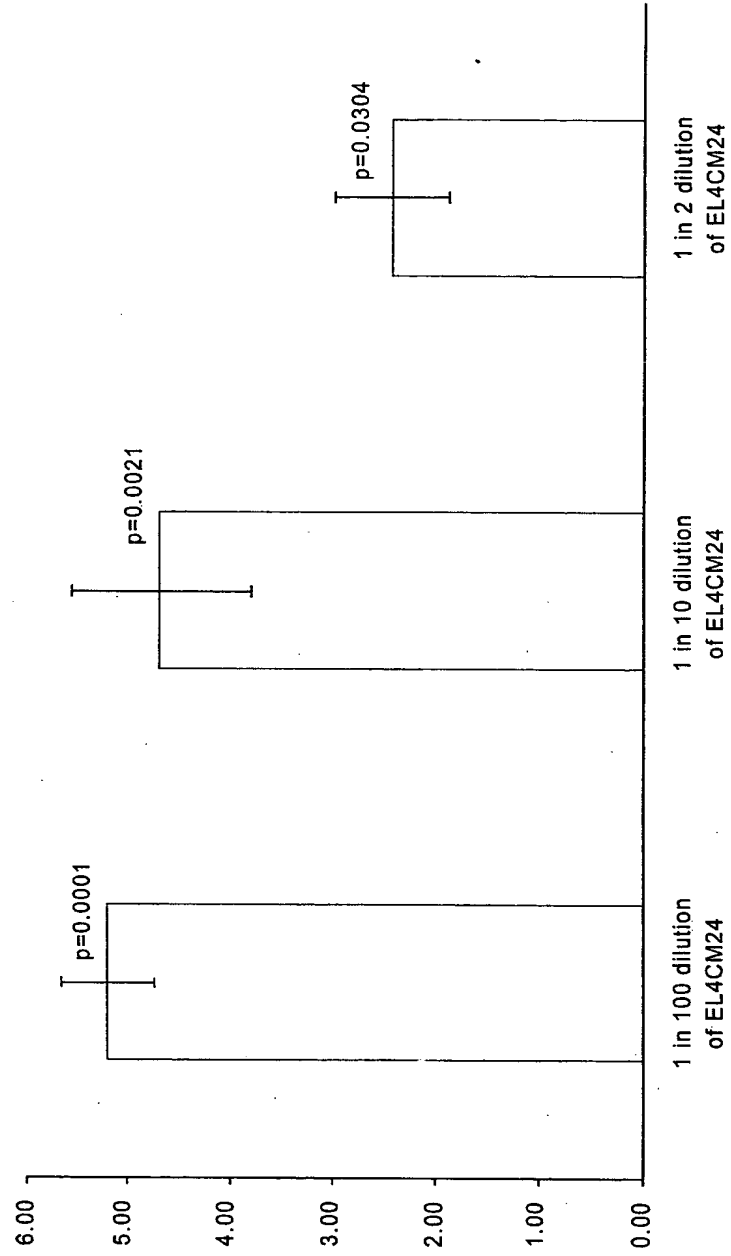


FIG. 3
Heat Inactivation and Proteinase K Digestion of EL4CM24

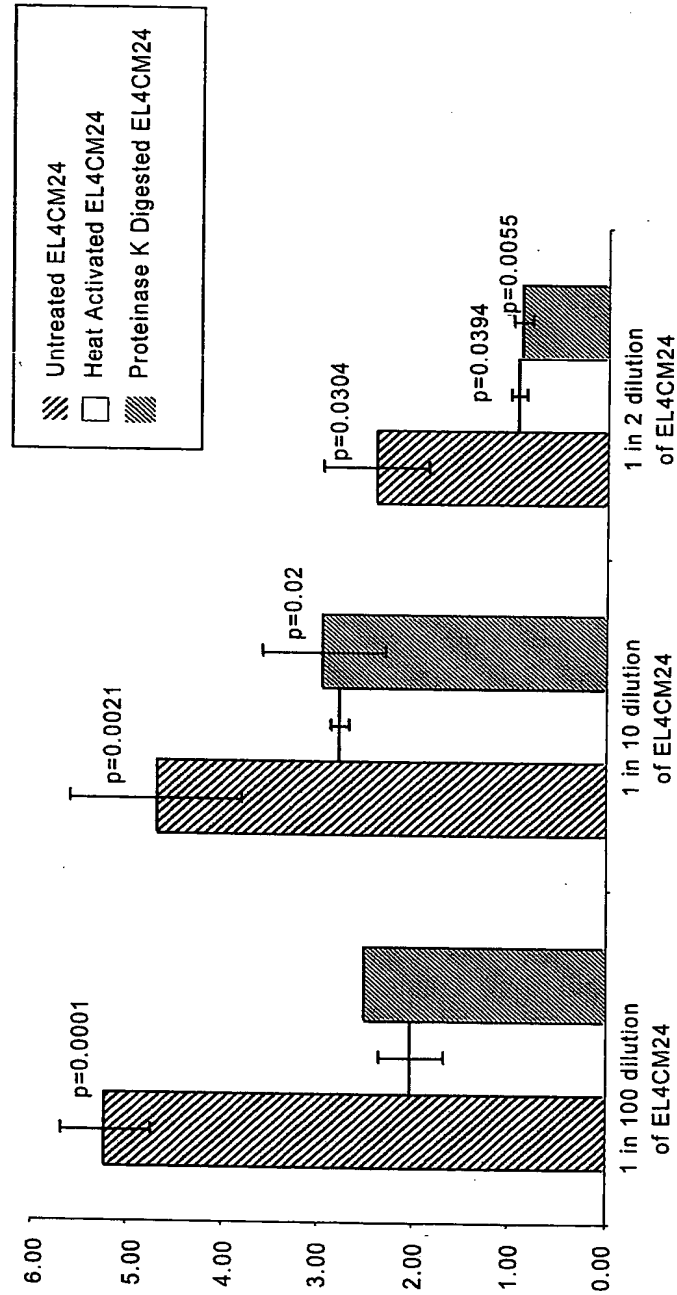
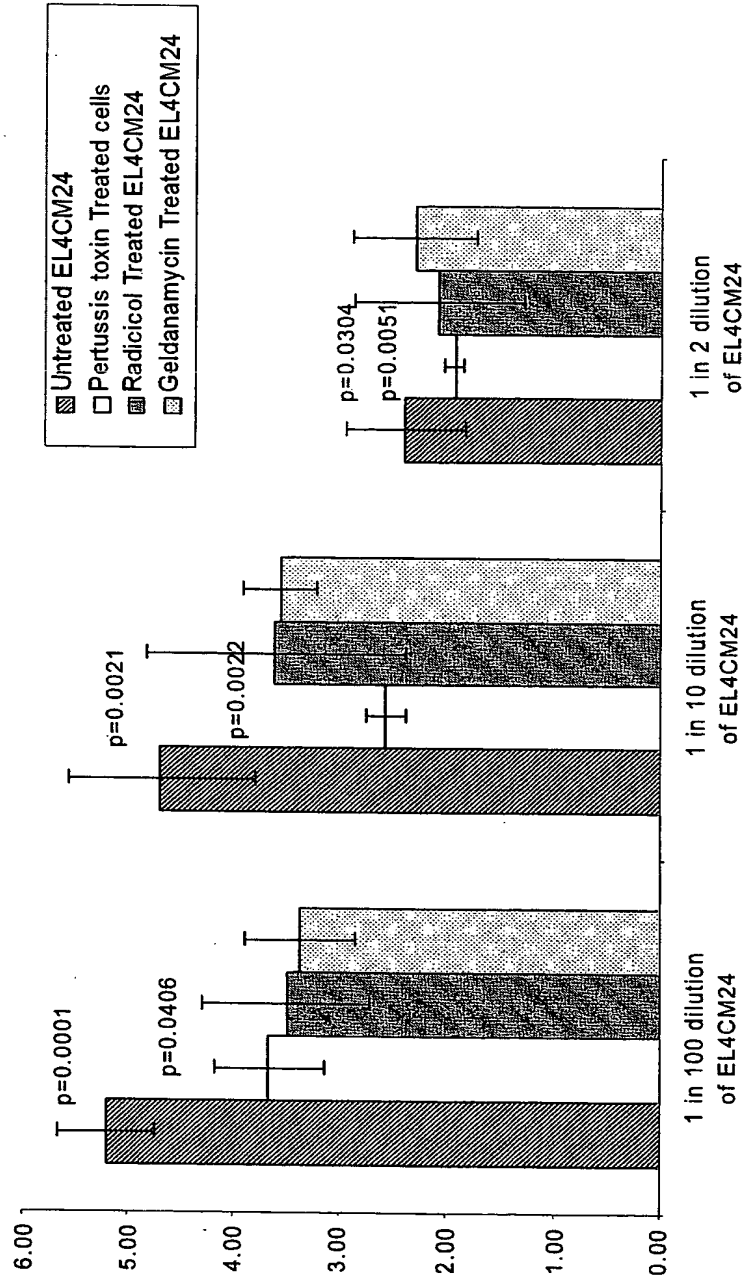


FIG. 4

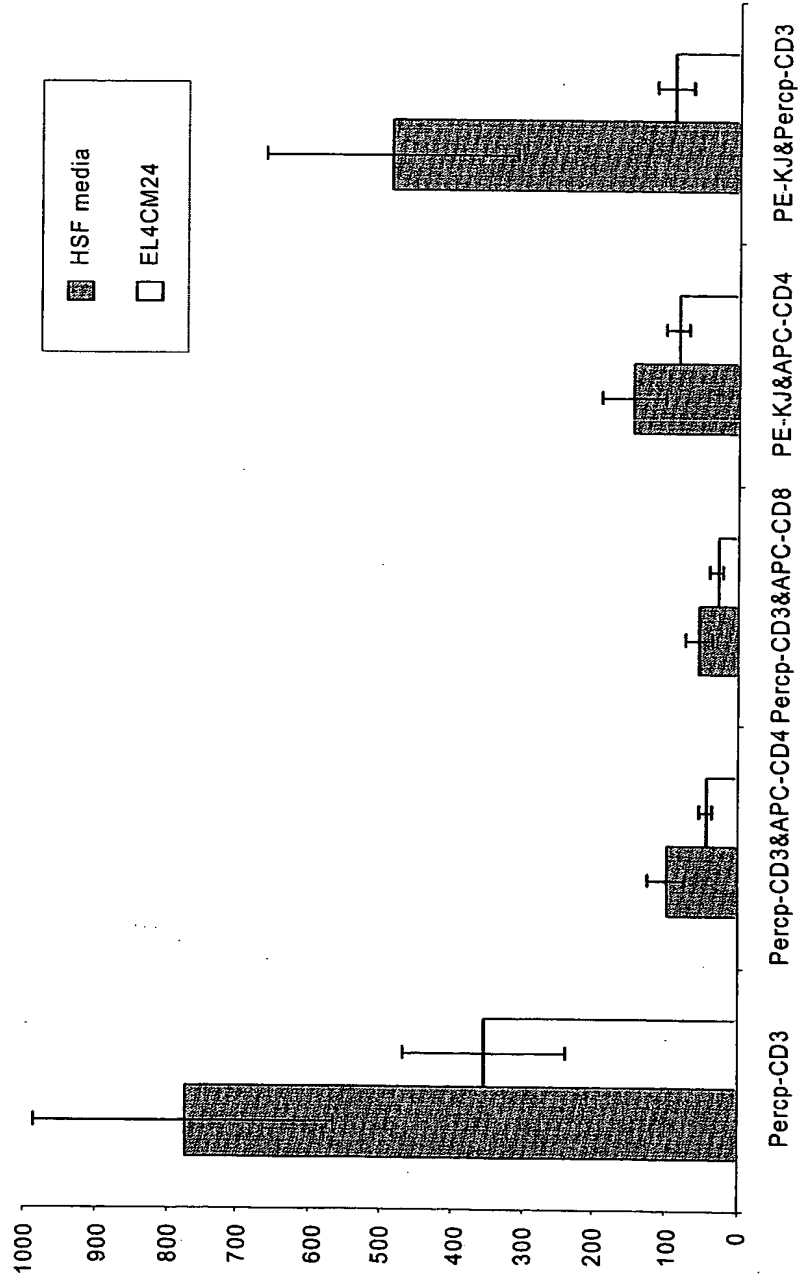
Use of Specific Inhibitors



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FIG. 5

EL4 Conditioned Media Repels T cells *in vivo*



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FIG. 6
EL4CM24 SDS PAGE

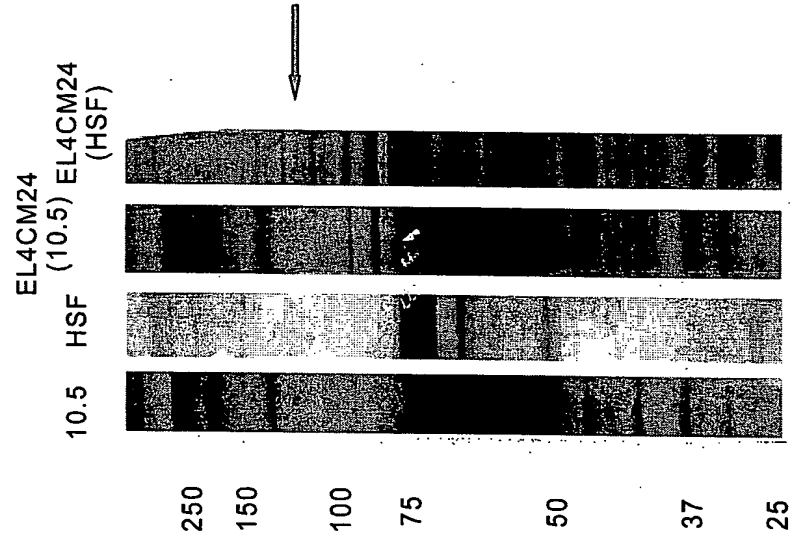
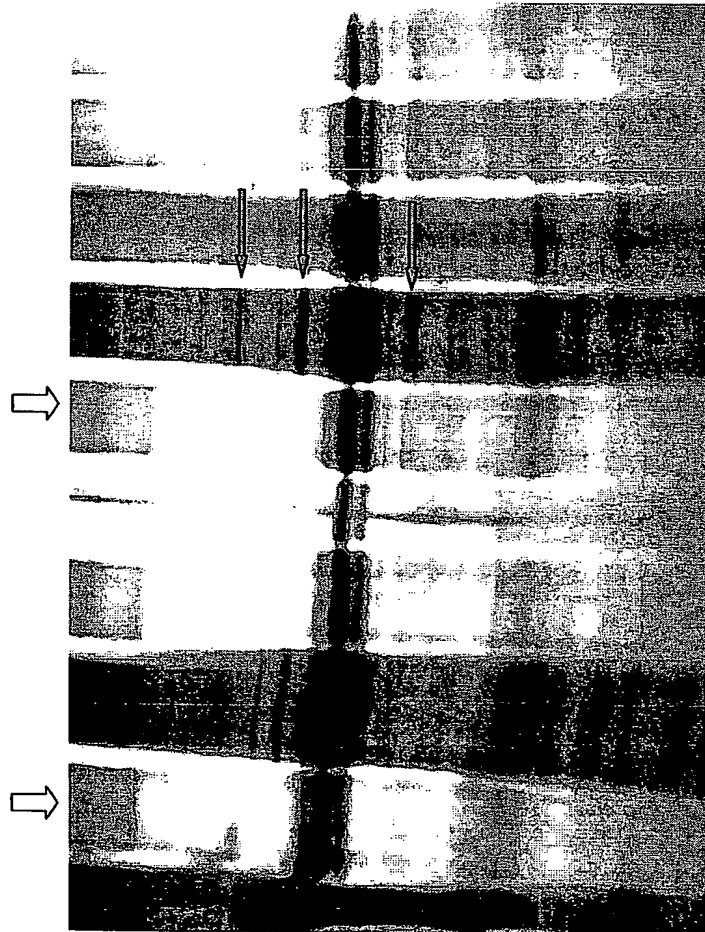


FIG. 7
Ion Exchange Chromatography

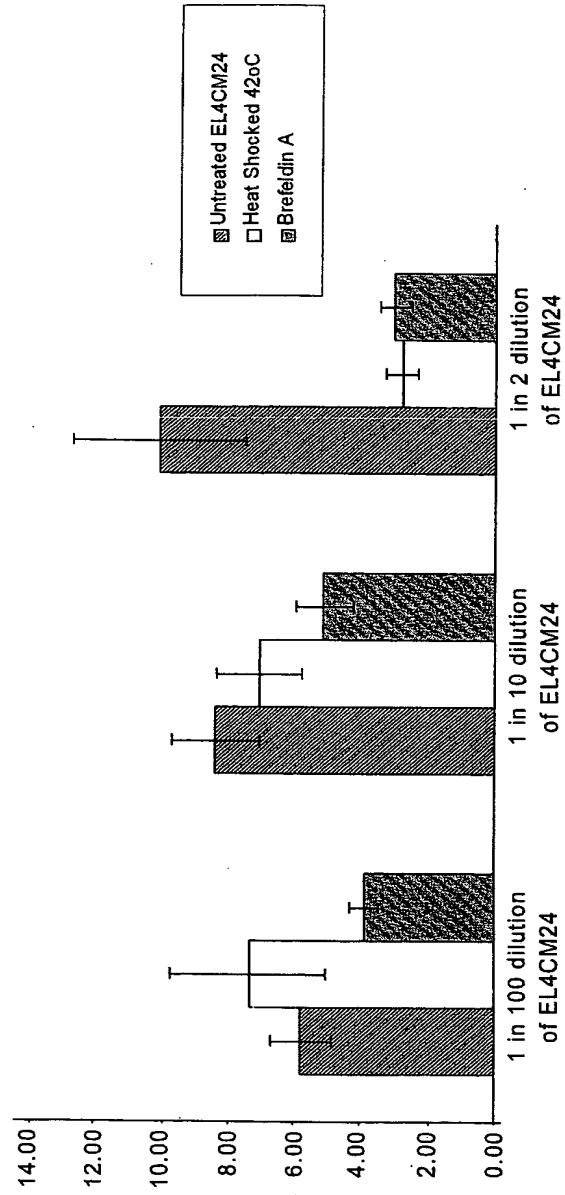


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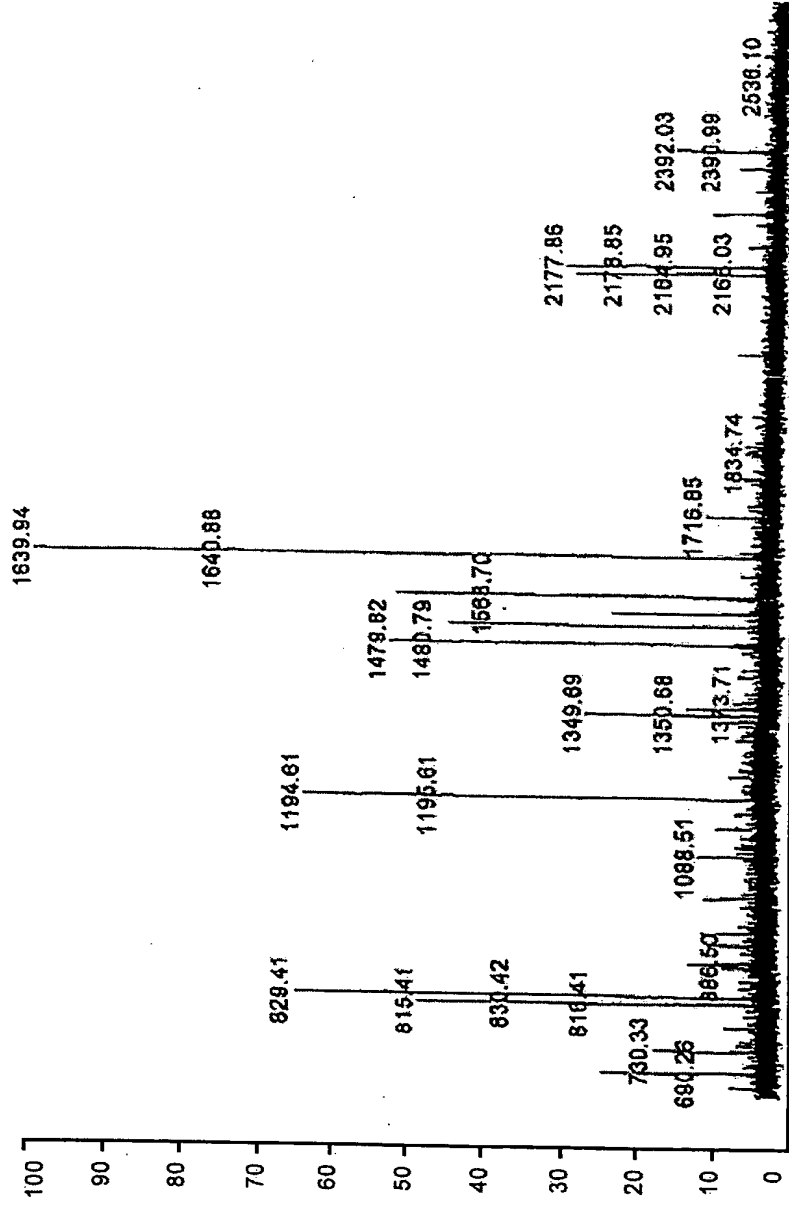
FIG. 8

Heat Shock of EL4 @ 42°C and Brefeldin A treatment of EL4



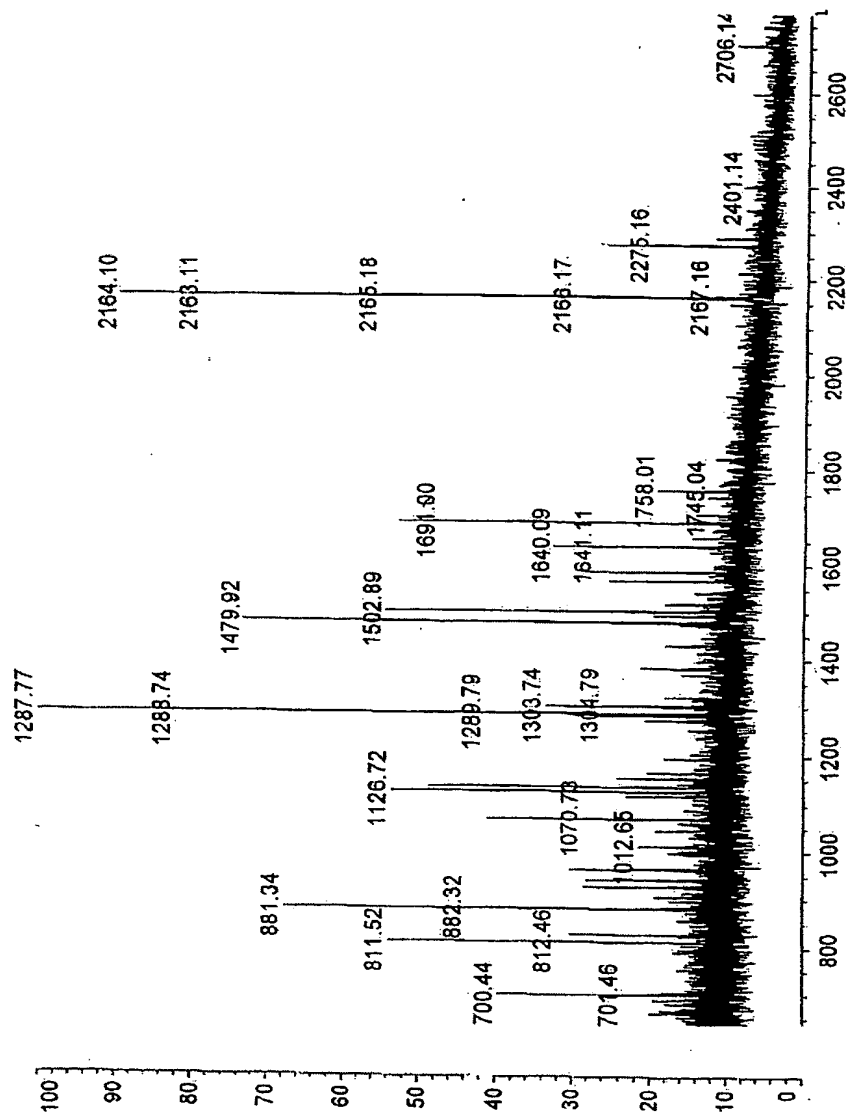
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FIG. 9



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FIG. 11



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FIG. 12A

MS-Fit Search Results

Press stop on your browser if you wish to abort this MS-Fit search prematurely.

Sample ID (comment): Magic Bullet digest

Database searched: NCBI nr.121002

Molecular weight search (1000 - 100000 Da) selects 1195692 entries.

Full pI range: 1247039 entries.

Species search (MAMMALS) selects 197947 entries.

Combined molecular weight, pI and species searches select 186900 entries.

MS-Fit search selects 407 entries (results displayed for top 4 matches).

Considered modifications: | Peptide N-terminal Gln to pyroGlu | Oxidation of M | Protein N-terminus Acetylated |

Min. # Peptides to Match	Peptide Mass Tolerance (+/-) ppm	Peptide Masses are monoisotopic	Digest Used Trypsin	Max. # Missed Cleavages 1	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O H)	Input # Peptide Masses 15
4	150.000							

Result Summary

Rank	MOWSE Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	NCBI nr.121002 Accession #	Protein Name
1	7.02e+003	8/15 (53%)	81963.2 / 4.99	EQUUS CABALLUS	20177936	heat shock protein 90 beta
2	6.91e+003	8/15 (53%)	83264.6 / 4.97	HOMO SAPIENS	20149594	Unknown (protein for MGC:1138)
3	6.79e+003	8/15 (53%)	84843.9 / 5.26	HOMO SAPIENS	11277141	hypothetical protein
4	2.25e+003	7/15 (46%)	83316.8 / 5.06	RATTUS SP.	1346320	heat shock protein 90; hsp90

Detailed Results

1. 8/15 matches (53%). 81963.2 Da, pI = 4.99. Acc. # 20177936. EQUUS CABALLUS. heat shock protein 90 beta .

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
689.3000	689.3946	-137.2410	570	575	(K)VTISNR(L)	
829.4100	829.5300	-144.6415	323	329	(R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	421	427	(K)FYEAFFSK(N)	
1194.6100	1194.6483	-32.0277	65	74	(K)IDIIPNPOER(T)	
1348.6900	1348.6650	18.5557	312	322	(K)HFSVEGOLEFR(A)	
1513.7800	1513.7862	-4.1036	371	384	(R)GVVDSEDLPLNISR(E)	
2176.8600	2176.9457	-39.3681	449	467	(R)YHTSQSGDEMTSLSEYVSR(M)	
2390.9900	2391.1832	-80.8096	474	494	(K)SIYYITGESKEOVANSAFVER(V)	

7 unmatched masses: 730.3300 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 13% (95/713 AA's) of the protein.
Coverage Map for This Hit (MS-Digest index #): 1205701

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FIG. 12B

2. 8/15 matches (53%). 83264.6 Da, pI = 4.97. Acc. # 20149594. HOMO SAPIENS. Unknown (protein for MGC:1138).

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
689.3000	689.3946	-137.2410	578	583	(K)VTISNR(L)	
829.4100	829.5300	-144.6415	331	337	(R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	429	435	(K)FYEAFSK(N)	
1194.6100	1194.6483	-32.0277	73	82	(K)IDHPNPOER(T)	
1348.6900	1348.6650	18.5557	320	330	(K)HFSVEGOLEFR(A)	
1513.7800	1513.7862	-4.1036	379	392	(R)GVYDSEDLPLNISR(E)	
2176.8600	2176.9457	-39.3681	457	475	(R)YHTSOSGDEMTSLSEYVSR(M)	
2390.9900	2391.1832	-80.8096	482	502	(K)SIYYITGESKEQVANSAFYER(V)	

7 unmatched masses: 730.3300 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 13% (95/724 AA's) of the protein.
Coverage Map for This Hit (MS-Digest index #): [137455](#)

3. 8/15 matches (53%). 84843.9 Da, pI = 5.26. Acc. # 11277141. HOMO SAPIENS. hypothetical protein.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
689.3000	689.3946	-137.2410	578	583	(K)VTISNR(L)	
829.4100	829.5300	-144.6415	331	337	(R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	429	435	(K)FYEAFSK(N)	
1194.6100	1194.6483	-32.0277	73	82	(K)IDHPNPOER(T)	
1348.6900	1348.6650	18.5557	320	330	(K)HFSVEGOLEFR(A)	
1513.7800	1513.7862	-4.1036	379	392	(R)GVYDSEDLPLNISR(E)	
2176.8600	2176.9457	-39.3681	457	475	(R)YHTSOSGDEMTSLSEYVSR(M)	
2390.9900	2391.1832	-80.8096	482	502	(K)SIYYITGESKEQVANSAFYER(V)	

7 unmatched masses: 730.3300 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 12% (95/737 AA's) of the protein.
Coverage Map for This Hit (MS-Digest index #): [1101236](#)

4. 7/15 matches (46%). 83316.8 Da, pI = 5.06. Acc. # 1346320. RATTUS SP.. heat shock protein 90: hsp90.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
689.3000	689.3946	-137.2410	578	583	(K)VTISNR(L)	
829.4100	829.5300	-144.6415	331	337	(R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	429	435	(K)FYEAFSK(N)	
1348.6900	1348.6650	18.5557	320	330	(K)HFSVEGOLEFR(A)	
1513.7800	1513.7862	-4.1036	379	392	(R)GVYDSEDLPLNISR(E)	
2176.8600	2176.9457	-39.3681	457	475	(R)YHTSOSGDEMTSLSEYVSR(M)	
2390.9900	2391.1832	-80.8096	482	502	(K)SIYYITGESKEQVANSAFYER(V)	

8 unmatched masses: 730.3300 815.4100 1194.6100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

MS-Tag Search Results

Press stop on your browser if you wish to abort this MS-Tag search prematurely.

Sample ID (comment): Apo A-1 1040 AKPVLEDLR

Database searched: NCBI nr. 121002

Full Molecular Weight range: 1247039 entries.

Full pI range: 1247039 entries.

Species search (MAMMALS) selects 197947 entries.

Number of sequences passing through parent mass filter: 4253

MS-Tag search selects 7 entries (results displayed for top 3 matches).

Parent mass: 1194.6100 (+/- 0.2000 Da)

Fragment ions used in search: 175.31, 212.00, 229.20, 342.62, 355.43, 512.43, 529.50, 626.31, 713.44, 740.58, 966.73 (+/- 0.50 Da)

Ion Types Considered: a b y o b l

Search Mode	Max. # Unmatched Ions	Peptide Masses are monoisotopic	Digest Used	Max. # Missed Cleavages	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O H)
Identify	1		Trypsin	1			

Result Summary

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBI nr. 121002 Accession #	Protein Name
1	0/11	(K)IDHPNPOER(T)	1194.6483	-0.0383	83325.7 / 4.97	MOUSE	123681	Heat shock protein HSP 90-beta (HSP 94) (Tumor specific transplantation 84 kDa antigen) (TSTA)
1	0/11	(K)IDHPNPOER(T)	1194.6483	-0.0383	83361.1 / 5.03	MUS MUSCULUS	6680305	heat shock protein, 84 kDa 1
1	0/11	(K)IDHPNPOER(T)	1194.6483	-0.0383	14066.4 / 4.64	HOMO SAPIENS	2351110	heat shock protein beta

FIG. 12C

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBI nr. Accession #	MS-Digest Index #	Protein Name			
1	9/11	(K) <u>IDILPNFOER</u> (T)	1194.6483	-0.0383	83325.7 / 4.97	MOUSE	<u>123681</u>	<u>318176</u>	Heat shock protein HSP 90-beta (HSP 84) (Tumor specific transplantation 84 kDa antigen) (TSTA)			
1	9/11	(K) <u>IDILPNQPER</u> (T)	1194.6483	-0.0383	83361.1 / 5.03	MUS MUSCULUS	<u>6680305</u>	<u>583990</u>	heat shock protein, 84 kDa 1			
<hr/>												
Fragment-ion (m/z)		175.31	212.00	229.20	342.62	355.43	512.43	529.50	626.31	723.44	740.58	966.73
Ion-type		y ₁	NP	b ₂	b ₃	PQE	y ₄ -NH ₃	y ₄	y ₅ -NH ₃	y ₆ -NH ₃	y ₆	y ₈
Delta Da		0.19	-0.10	0.08 D1	0.42 DIL	0.27	0.18	0.23	0.02	0.10	0.21	0.19
				0.08	0.42							
1	9/11	(K) <u>IDILPNQPER</u> (T)	1194.6483	-0.0383	14066.4 / 4.64	HOMO SAPIENS	<u>235110</u>	<u>587097</u>	heat shock protein beta			
<hr/>												
Fragment-ion (m/z)		175.31	212.00	229.20	342.62	355.43	512.43	529.50	626.31	723.44	740.58	966.73
Ion-type		y ₁	NP	b ₂	b ₃	PQE	y ₄ -NH ₃	y ₄	y ₅ -NH ₃	y ₆ -NH ₃	y ₆	y ₈
Delta Da		0.19	-0.10	0.08 D1	0.42 DII	0.27	0.18	0.23	0.02	0.10	0.21	0.19
				0.08	0.42							

MS-Tag Search Results

Press stop on your browser if you wish to abort this MS-Tag search prematurely.

Sample ID (comment): Apo A-1 1040 AKPVLEDLR

Database searched: NCBI nr.121002

Molecular weight search (1000 - 100000 Da) selects 1195692 entries.
Full of masses: 1247030 entries

Full pl range: 1247039 entries.

Species search (MAMMALS) selects 197947 entries:

Combined molecular weight, pI and species searches select 186900 entries.
Number of sequences missing from the database is 10000.

MS-Tag search selects 18 entries (multiple identified from 1)

MS-Tag search selects 18 entries (results displayed for top 3 matches).

Parent mass: 815.4100 (+/- 0.2000 Da)

Fragment Ions used in search: 185.26, 255.27, 272.34, 298.32, 354.45, 371.53, 417.39, 445.25, 518.35 (+/- 0.50 Da)

Ion Types Considered: n b B y n b I

Search Mode identity	Max. # Unmatched Ions 1	Peptide Masses are monoisotopic	Digest Used Trypsin	Max. # Missed Cleavages 1	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O H)
----------------------------	----------------------------------	---------------------------------------	---------------------------	---------------------------------	--	---------------------------------------	--

Result Summary

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBI/Ref.121002 Accession #	Protein Name
1	0/9	(R)ALLFVPR(R)	815.5143	-0.1043	75541.0 / 5.28	MUS MUSCULUS	20892565	similar to heat shock protein 86
1	0/9	(R)ALLFVPR(R)	815.5143	-0.1043	84674.2 / 4.94	HOMO SAPIENS	123678	90 kDa heat-shock protein (AA 1-732)
1	0/9	(K)ALLFVPR(R)	815.5143	-0.1043	57068.0 / 6.38	HOMO SAPIENS	12804541	hypothetical protein LOC63929

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁻ Error (Da)	Protein MW (Da)/pI	Species	NCBI nr.121002 Accession #	MS-Digest Index #	Protein Name	
1	0/9	(R) <u>A</u> LLFVPR(R)	815.5143	-0.1043	75541.0 / 5.28	MUS MUSCULUS	<u>2088256S</u>	<u>613811</u>	similar to heat shock protein 86	
1	0/9	(R) <u>A</u> LLFVPR(R)	815.5143	-0.1043	84674.2 / 4.94	HOMO SAPIENS	<u>123678</u>	<u>162860</u>	90 kDa heat-shock protein (AA 1-732)	
<hr/>										
Fragment-ion (m/z)		185.26	255.27	272.34	298.32	354.45	371.53	417.39	445.25	518.35
Ion-type		b ₁	y ₂ -NH ₃	y ₂	b ₃	y ₃ -NH ₃	y ₃	a ₄	d ₄	y ₄
Delta Da		0.13	0.12	0.17	0.11	0.24	0.29	0.10	-0.03	0.04
<hr/>										
1	0/9	(K) <u>A</u> LLFVPR(R)	815.5143	-0.1043	57068.0 / 6.38	HOMO SAPIENS	<u>12804541</u>	<u>171353</u>	hypothetical protein LOC63929	
<hr/>										
Fragment-ion (m/z)		185.26	255.27	272.34	298.32	354.45	371.53	417.39	445.25	518.35
Ion-type		b ₁	y ₂ -NH ₃	y ₂	b ₃	y ₃ -NH ₃	y ₃	a ₄	b ₄	y ₄
Delta Da		0.13	0.12	0.17	0.11	0.24	0.29	0.10	-0.03	0.04

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FIG. 13A

MS-Fit Search Results

Press stop on your browser if you wish to abort this MS-Fit search prematurely.

Sample ID (comment): Magic Bullet digest

Database searched: NCBI nr.51403

Molecular weight search (1000 - 200000 Da) selects 1421445 entries.

Full pI range: 1432416 entries.

Species search (HUMAN RODENT) selects 224838 entries.

Combined molecular weight, pI and species searches select 222557 entries.

MS-Fit search selects 5 entries (results displayed for top 3 matches).

Considered modifications: | Peptide N-terminal Gln to pyroGlu | Oxidation of M | Protein N-terminus Acetylated |

Min. # Peptides to Match	Peptide Mass Tolerance (+/-) ppm	Peptide Masses are monoisotopic	Digest Used Trypsin	Max. # Missed Cleavages	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O H)	Input # Peptide Masses
7	150.000			1				13

Result Summary

Rank	MOWSE Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	NCBI nr.51403 Accession #	Protein Name
1	1.81e+003	7/13 (53%)	94057.0 / 5.13	RATTUS NORVEGICUS	24025637	ischemia responsive 94 kDa protein
2	449	7/13 (53%)	94081.1 / 5.13	MUS MUSCULUS	13277753	heat shock protein 4
2	449	7/13 (53%)	94133.1 / 5.15	MUS MUSCULUS	6680301	apg-2

Detailed Results

1. 7/13 matches (53%). 94057.0 Da, pI = 5.13. Acc. # 24025637. RATTUS NORVEGICUS. ischemia responsive 94 kDa protein.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
798.5500	798.4514	123.4893	431	436	(K)VLTFYR(K)	
949.6100	949.5219	92.7425	62	69	(K)NTVQGFKR(F)	
1321.8500	1321.7116	104.7200	222	234	(K)VLATAFDITLGGK(K)	
1402.7800	1402.6313	106.0213	619	629	(K)NAVEEYVEMR(D)	
1495.8400	1495.7029	91.6785	20	33	(R)AGGIETIANEYSDR(C)	
1736.0700	1735.9271	82.3407	391	405	(R)EFSITDVVPYFISLR(W)	
1953.0400	1952.8336	105.6759	406	422	(R)WNSPAEEGSSDCEVFPK(N)	

6 unmatched masses: 915.6000 917.3600 1305.8400 1478.8800 1587.9500 1624.0500

The matched peptides cover 10% (84/840 AA's) of the protein.
Coverage Map for This Hit (MS-Digest Index #): [787619](#)

2. 7/13 matches (53%). 94081.1 Da, pI = 5.13. Acc. # 13277753. MUS MUSCULUS. heat shock protein 4.

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FIG. 13B

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
798.5500	798.4514	123.4893	431	436	(K) <u>VLTFYR</u> (K)	
949.6100	949.5219	92.7425	62	69	(K) <u>NTVOGFKR</u> (F)	
1305.8400	1305.7418	75.1849	670	680	(K) <u>QVYVDKLAELK</u> (S)	
1321.8500	1321.7116	104.7200	222	234	(K) <u>VLATAFDITLGGR</u> (K)	
1402.7800	1402.6313	106.0213	620	630	(K) <u>NAVEEYVYEMR</u> (D)	
1495.8400	1495.7029	91.6785	20	33	(R) <u>AGGIETIANEYSDR</u> (C)	
1736.0700	1735.9271	82.3407	391	405	(R) <u>EFSITDVVPYPISLR</u> (W)	

6 unmatched masses: 915.6000 917.3600 1478.8800 1587.9500 1624.0500 1953.0400

The matched peptides cover 9% (78/841 AA's) of the protein.
Coverage Map for This Hit (MS-Digest index #): 202745

2. 7/13 matches (53%). 94133.1 Da, pI 5.15, Acc. # 6680301, MUS MUSCULUS, apg-2.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
798.5500	798.4514	123.4893	431	436	(K) <u>VLTFYR</u> (K)	
949.6100	949.5219	92.7425	62	69	(K) <u>NTVOGFKR</u> (F)	
1305.8400	1305.7418	75.1849	670	680	(K) <u>QVYVDKLAELK</u> (S)	
1321.8500	1321.7116	104.7200	222	234	(K) <u>VLATAFDITLGGR</u> (K)	
1402.7800	1402.6313	106.0213	620	630	(K) <u>NAVEEYVYEMR</u> (D)	
1495.8400	1495.7029	91.6785	20	33	(R) <u>AGGIETIANEYSDR</u> (C)	
1736.0700	1735.9271	82.3407	391	405	(R) <u>EFSITDVVPYPISLR</u> (W)	

6 unmatched masses: 915.6000 917.3600 1478.8800 1587.9500 1624.0500 1953.0400

The matched peptides cover 9% (78/841 AA's) of the protein.
Coverage Map for This Hit (MS-Digest index #): 1179227

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FIG. 14A

MS-Fit Search Results

Press stop on your browser if you wish to abort this MS-Fit search prematurely.

Sample ID (comment): Magic Bullet digest

Database searched: NCBI nr.51403

Molecular weight search (1000 - 100000 Da) selects 1372760 entries.

Full pI range: 1432416 entries.

Species search (HUMAN RODENT) selects 224838 entries.

Combined molecular weight, pI and species searches select 211465 entries.

MS-Fit search selects 335 entries (results displayed for top 3 matches).

Considered modifications: | Peptide N-terminal Gln to pyroGlu | Oxidation of M | Protein N-terminus Acetylated |

Min. # Peptides to Match	Peptide Mass Tolerance (+/-) ppm	Peptide Masses are monoisotopic	Digest Used Trypsin	Max. # Missed Cleavages	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O H)	Input # Peptide Masses 17
4	150,000			1				

Result Summary

Rank	MOWSE Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	NCBI nr.51403 Accession #	Protein Name
1	1.22e+005	11/17 (64%)	70149.7 / 5.20	MUS MUSCULUS	<u>29840803</u>	unnamed protein product
2	1.22e+005	11/17 (64%)	70163.8 / 5.24	MUS MUSCULUS	<u>26326929</u>	unnamed protein product
3	2.66e+004	10/17 (58%)	70201.8 / 5.28	MUS MUSCULUS	<u>6679385</u>	65-kDa macrophage protein

Detailed Results

1. 11/17 matches (64%). 70149.7 Da, pI = 5.20. Acc. # 29840803. MUS MUSCULUS. unnamed protein product .

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
700.4400	700.4146	36.2352	77	82	(K)VFHGLK(S)	
811.5200	811.4136	131.0872	585	591	(K)YAI SMAR(K)	
942.5800	942.5413	41.0831	442	449	(R)Y NKPPYPK(L)	
1069.7200	1069.6257	88.1285	264	272	(K)LSPEELL LR(W)	
1126.7200	1126.6373	73.4015	433	441	(K)IKVPVDWNR(V)	
1135.7100	1135.6111	87.0474	348	357	(R)QFVTATDVVR(G)	
1287.7700	1287.6268	111.2008	402	412	(R)NWMNSLG VNPR(V)	
1502.8900	1502.7525	91.5194	166	178	(K)MINLSVPI TIDER(T)	
1585.9400	1585.8477	58.1710	597	610	(R)VYALPEDLVEV NPK(M)	
1689.9700	1689.8560	67.4478	473	488	(K)FSLVGIACQDLNEGNR(T)	
1758.0100	1757.8744	77.1528	310	326	(K)GDFEGIPAVVIDMSCLR(E)	

6 unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900

The matched peptides cover 19% (120/627 AA's) of the protein.

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FIG. 14B

Coverage Map for This Hit (MS-Digest index #): 372720

2. 11/17 matches (64%). 70163.8 Da, pI = 5.24. Acc. # 26326929. MUS MUSCULUS. unnamed protein product.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
700.4400	700.4146	36.2352	77	82	(K) <u>VFHGLK</u> (S)	
811.5200	811.4136	131.0872	585	591	(K) <u>YAISMAR</u> (K)	
942.5800	942.5413	41.0831	442	449	(R) <u>VNKPPYPK</u> (L)	
1069.7200	1069.6257	88.1285	264	272	(K) <u>LSPEELLR</u> (W)	
1126.7200	1126.6373	73.4015	433	441	(K) <u>IKVPVDWNR</u> (V)	
1135.7100	1135.6111	87.0474	348	357	(R) <u>QFVTATDVVR</u> (G)	
1287.7700	1287.6268	111.2008	402	412	(R) <u>NWMNSLGVNPR</u> (V)	
1502.8900	1502.7525	91.5194	166	178	(K) <u>MINLSVPTIDER</u> (T)	
1585.9400	1585.8477	58.1710	597	610	(R) <u>VYALPEDLVEVNP</u> (M)	
1689.9700	1689.8560	67.4478	473	488	(K) <u>FSLVGIACODLNEG</u> (T)	
1758.0100	1757.8744	77.1528	310	326	(K) <u>GDEEGIPAVVIDMSGLR</u> (E)	

6 unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900

The matched peptides cover 19% (120/627 AA's) of the protein.

Coverage Map for This Hit (MS-Digest index #): 1174311

3. 10/17 matches (58%). 70201.8 Da, pI = 5.28. Acc. # 6679385. MUS MUSCULUS. 65-kDa macrophage protein.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence (Click for Fragment Ions)	Modifications
700.4400	700.4146	36.2352	77	82	(K) <u>VFHGLK</u> (T)	
811.5200	811.4136	131.0872	585	591	(K) <u>YAISMAR</u> (K)	
942.5800	942.5413	41.0831	442	449	(R) <u>VNKPPYPK</u> (L)	
1069.7200	1069.6257	88.1285	264	272	(K) <u>LSPEELLR</u> (W)	
1126.7200	1126.6373	73.4015	433	441	(K) <u>IKVPVDWNR</u> (V)	
1135.7100	1135.6111	87.0474	348	357	(R) <u>QFVTATDVVR</u> (G)	
1287.7700	1287.6268	111.2008	402	412	(R) <u>NWMNSLGVNPR</u> (V)	
1502.8900	1502.7525	91.5194	166	178	(K) <u>MINLSVPTIDER</u> (T)	
1585.9400	1585.8477	58.1710	597	610	(R) <u>VYALPEDLVEVNP</u> (M)	
1758.0100	1757.8744	77.1528	310	326	(K) <u>GDEEGIPAVVIDMSGLR</u> (E)	

7 unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900 1689.9700

The matched peptides cover 16% (104/627 AA's) of the protein.

Coverage Map for This Hit (MS-Digest index #): 746520

FIG. 14C

MS-Tag Search Results

Press stop on your browser if you wish to abort this MS-Tag search prematurely.

Sample ID (comment): Apo A-1 1040 AKPVLEDLR

Database searched: NCBI nr.51403

Molecular weight search (1000 - 200000 Da) selects 1421445 entries.

Full pI range: 1432416 entries.

Species search (HUMAN RODENT) selects 224838 entries.

Combined molecular weight, pI and species searches select 222557 entries.

Number of sequences passing through parent mass filter: 4727

MS-Tag search selects 6 entries.

Parent mass: 1287.7700 (+/- 0.2000 Da)

Fragment ions used in search: 175.00, 255.28, 272.30, 301.48, 369.37, 432.69, 542.65, 633.34, 655.97, 742.67, 840.69 (-/- 0.70 Da)

Ion Types Considered: a b B y n h

Search Mode	Max. # Unmatched Ions	Peptide Masses are monoisotopic	Digest Used Trypsin	Max. # Missed Cleavages	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O H)
identity	2			1			

Result Summary

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBI nr.51403 Accession #	Protein Name
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70288.8 / 5.29	HOMO SAPIENS	8217500	bA139H14.1 (lymphocyte cytosolic protein 1 (L-plastin))
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70289.7 / 5.20	HOMO SAPIENS	4504965	lymphocyte cytosolic protein 1 (L-plastin)
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70201.8 / 5.28	MUS MUSCULUS	6679385	65-kDa macrophage protein
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	32331.4 / 8.60	MUS MUSCULUS	12843863	unnamed protein product
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70163.8 / 5.24	MUS MUSCULUS	26326929	unnamed protein product
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70149.7 / 5.20	MUS MUSCULUS	29840803	unnamed protein product

Detailed Results

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBI nr.51403 Accession #	MS-Digest Index #	Protein Name
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70288.8 / 5.29	HOMO SAPIENS	8217500	696262	bA139H14.1 (lymphocyte cytosolic protein 1 (L-plastin))
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70289.7 / 5.20	HOMO SAPIENS	4504965	725402	lymphocyte cytosolic protein 1 (L-plastin)
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70201.8 / 5.28	MUS MUSCULUS	6679385	746520	65-kDa macrophage protein
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	32331.4 / 8.60	MUS MUSCULUS	12843863	1146923	unnamed protein product
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70163.8 / 5.24	MUS MUSCULUS	26326929	1174311	unnamed protein product
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70149.7 / 5.20	MUS MUSCULUS	29840803	372720	unnamed protein product

Fragment-ion (m/z)	175.00	255.28	272.30	301.48	369.37	432.69	542.65	633.34	655.97	742.67	840.69
Ion-type	y ₁	y ₂ -NH ₃	y ₂	b ₂	y ₃ -NH ₃	b ₃	y ₅	b ₅	y ₆	y ₇	
Delta Da	-0.12	0.13	0.13	0.35	0.18	0.52	0.34	0.09	0.58	0.25	

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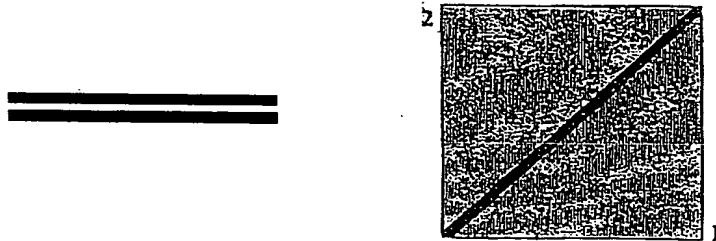
FIG. 15A

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Matrix: BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.00 wordsize: 3 Filter ☒

Sequence 1 gi 72220 heat shock protein 86 - mouse Length 733 (1 .. 733)

Sequence 2 gi 72223 heat shock protein 84 - mouse Length 724 (1 .. 724)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1102 bits (2851), Expect = 0.0

Identities = 564/733 (76%), Positives = 611/733 (82%), Gaps = 9/733 (1%)

```
Query: 1  MPEETQTQDQPMEEEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIR 60
          MPEE                      EEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISN+SDALDKIR
Sbjct: 1  MPPEVHNG-----EEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNASDALDKIR 55

Query: 61  YESLTDPSKLD SGKELHINLIPSKQDRITLIVDTGIGMTKADLINNLGTIAKSGTKAFME 120
          YESLTDPSKLD SGKEL I++IP+ Q+RTLT+VDTGIGMTKADLINNLGTIAKSGTKAFME
Sbjct: 56  YESLTDPSKLD SGKELKIDIIPNPQERTLTIVDTGIGMTKADLINNLGTIAKSGTKAFME 115

Query: 121  ALQAGADISMIGQFGVGFYSAYLVAEKVTVITKHNDDEQYAWESSAGGSFTVRDGTGPEM 180
          ALQAGADISMIGQFGVGFYSAYLVAEKV VITKHNDDEQYAWESSAGGSFTVR D GEP+
Sbjct: 116  ALQAGADISMIGQFGVGFYSAYLVAEKVVVITKHNDDEQYAWESSAGGSFTVRADHGEPI 175

Query: 181  GRGTVILHLKEDQTEYLEERRIKEIVKHSQFIGYPITLFEKERXXXXXXXXXXXXXXXXX 240
          GRGTVILHLKEDQTEYLEERR+KE+VKHSQFIGYPITL++EKER
Sbjct: 176  GRGTVILHLKEDQTEYLEERRVKEVVKHSQFIGYPITLYLEKEREKEISDDEAEEEKG 235

Query: 241  XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 300
          LNKTKPIWTR
Sbjct: 236  EKEEDKEDEEKPKIEDVGSDEEDDSGKKKKKTKKIKEYIDQEE---LNKTKPIWTR 291

Query: 301  NPDDITNBEYGEFYKSLTNDWEEHLAVKHFSVEGQLEFRALLFVPRRAPFDLPENRKKKN 360
          NPDDIT EEYGEFYKSLTNDWE+HLAVKHFSVEGQLEFRALLF+PRRAPFDLPEN+KKKN
Sbjct: 292  NPDDITQEEYGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFIPRRAPFDLPENKKKKKN 351

Query: 361  NIKLYVRRVFI MDNCEELIPEYLNFI RGVVDS EDLP LNISREMLQQSKILKVIRKNLVKK 420
```

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FIG. 15B

NIKLYVRRVFIMD+C+ELI LNFIKGVVDSDELPLNISREMLQOSKILKVI VVKK
 Sbjct: 352 NIKLYVRRVFIMDSCDELIHEYLNFIKGVVDSDELPLNISREMLQOSKILKVIKVNIVKK 411
 Query: 421 CLELFTELAEDKENYKKFYEQFSKNIKLGIHEDSQNRKCLSELLRYTSASGDEMVS LKD 480
 CLELF+ELAEDKENYKKFYE FSKN+KLG IHEDS NR++LSELLRY+TS SGDEM SL +
 Sbjct: 412 CLELFSELAEDKENYKKFYEA FSKVLKLG IHEDSTNRRRLSELLRYHTSQSGDEMTSLSE 471
 Query: 481 YCTRMKENQKHIFITGETKDQVANS AFVERLRKHCL EVIYMI EPIDEYCVQQLKEFEGK 540
 Y +RMKE OK IY+ITGE+K+QVANS AFVER+RK G EV+YM EPIDEYCVQQLKEF+GK
 Sbjct: 472 YVSRMKETQKSIYYITGESKEQVANS AFVERVRKRGFEVVMTEPIDEYCVQQLKEFDGK 531
 Query: 541 TLVSVTXXXXXXXXXXXXXXXXXXXXXXXXXNLCKIMKDILEKKVEKV VVSNRLVTSPCCI 600
 +LVSVT NLCK+MK+IL+KKVEKV +SNRLV+SPCCI
 Sbjct: 532 SLVSVTKEGLELPEDEEEKKMEESKAKFENLCKLMKEILDKKVEKVTISNRLVSSPCCI 591
 Query: 601 VTSTYGWTANMERIMKAQALRDNSTMGYMAAKIGHLEINPDHSIIETLRQKAEADKNDKSV 660
 VTSTYGWTANMERIMKAQALRDNSTMGYM AKKHL EINPDH I+ETLRQKAEADKNDK+V
 Sbjct: 592 VTSTYGWTANMERIMKAQALRDNSTMGYMAAKIGHLEINPDHPIVETLRQKAEADKNDKAV 651
 Query: 661 KDLVILLYETALLSSGFSLEDPQTHANRIYRM IKLGLGIDEDDPTVDDTSAAVTEEMPPL 720
 KDLV+LL+ETALLSSGFSLEDPQTH+NRIYRM IKLGLGIDED+ T ++ SAAV +E+PPL
 Sbjct: 652 KDLVVLLFETALLSSGFSLEDPQTHSNRIYRM IKLGLGIDEDEVTAEPSSAAVPDEIPPL 711
 Query: 721 EGDDDTSRMEEVD 733
 EGD+D SRMEEVD
 Sbjct: 712 EGDEDASRMEEVD 724

CPU time: 0.17 user secs. 0.01 sys. secs 0.18 total secs.

Lambda K H
 0.316 0.134 0.372

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 5349
 Number of Sequences: 0
 Number of extensions: 384
 Number of successful extensions: 3
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1
 length of query: 733
 length of database: 405,742,523
 effective HSP length: 134
 effective length of query: 599
 effective length of database: 405,742,389
 effective search space: 243039691011
 effective search space used: 243039691011
 T: 9
 A: 40
 X1: 16 (7.3 bits)
 X2: 129 (49.7 bits)
 X3: 129 (49.7 bits)
 S1: 41 (21.6 bits)
 S2: 78 (34.7 bits)

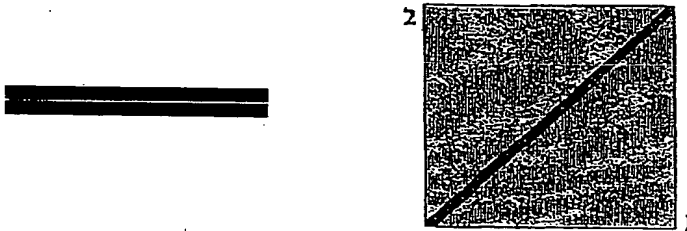
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FIG. 16A

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.00** wordsize: **3** Filter **F**

Sequence 1 gi 72220 heat shock protein 86 - mouse Length 733 (1 .. 733)

Sequence 2 gi 72223 heat shock protein 84 - mouse Length 724 (1 .. 724)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1102 bits (2851), Expect = 0.0

Identities = 564/733 (76%), Positives = 611/733 (82%), Gaps = 9/733 (1%)

```

Query: 1  MPEETQTQDQPMEEEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIR 60
          MPEE                      EEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELIS+SDALDKIR
Sbjct: 1  MPEEVHGG-----EEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNASDALDKIR 55

Query: 61  YESLTDPSKLDGKELHINLIPSKQDRTLTIVDTGIGMTKADLINNLGTIAKSGTKAFME 120
          YESLTDPSKLDGKEL I+IP+ Q+RTLT+VDTGIGMTKADLINNLGTIAKSGTKAFME
Sbjct: 56  YESLTDPSKLDGKELKIDIIPNPQERTTLTLVDTGIGMTKADLINNLGTIAKSGTKAFME 115

Query: 121  ALQAGADISMIGQFGVGFYSAYLVAEKVTVITKHNDDEQYAWESSAGGSFTVRDGTGEPM 180
          ALQAGADISMIGQFGVGFYSAYLVAEKV VITKHNDDEQYAWESSAGGSFTVR D GEP+
Sbjct: 116  ALQAGADISMIGQFGVGFYSAYLVAEKVVVITKHNDDEQYAWESSAGGSFTVRADHGEPI 175

Query: 181  GRGTKVILHLKEDQTEYLEERRIKEIVKHSQFIGYPITLFVEKERXXXXXXXXXXXXXXXXX 240
          GRGTKVILHLKEDQTEYLEERR+KE+VKHSQFIGYPITL++EKEK
Sbjct: 176  GRGTKVILHLKEDQTEYLEERRVKEVVKHSQFIGYPITLYLEKEREREISDDEAEBEKG 235

Query: 241  XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 300
          LNKTKPIWTR
Sbjct: 236  EKEEDKEDEEKPKIEDVGSDEEDDSGDKKKKTKKIKKEYIDQEE----LNKTKPIWTR 291

Query: 301  NPDDITNEEYGEFYKSLTNDWEHLAVGHFSVEGQLEFRALLFVPRRAPFDLFENRKKKN 360
          NPDDIT EEEYGEFYKSLTNDWE+HLAVKHFSVEGQLEFRALLF+PRRAPFDLFEN+KKKN
Sbjct: 292  NPDDITQEEYGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFIPRRAPFDLFENKKKKN 351

Query: 361  NIKLYVRRVFIMDNCEELIPEYLNFIIRGVVDSDELPLNISREMLQQSKILKVIRKQNLVKK 420

```


FIG. 16B

```

NIMLYVRRVFIND+C+EL+ LNFIQGVVSEDLPLNISREMLQOSKILKVI +VKK
Sbjct: 352 NIMLYVRRVFINDSCDELIBEYLNFIQGVVSEDLPLNISREMLQOSKILKVI+ANIVKK 411
Query: 421 CCELFTELARDKENYKKFYEQPSKXIKLGIHEDSQNRQCLSELLRYTTSAGDEMVSLEK 480
      CLELF+ELAEDKENYKKFYEQPSKXIKLGIHEDS NR++LSELLRY+TS SGOEM SL +
Sbjct: 412 CCELPSELAEDKENYKKFYEQPSKXIKLGIHEDSTNRRRLSELLRYHTSQSODENTSLSL 471
Query: 481 YCTRMKENGKHIYFITGETKQVANSATVERLRKHCLEVIYMIPIDEYCVQQLKEFEGR 540
      Y+RMKE QK IY+ITGE-X+QVANSATVER-RK G-EV-YM EPIDEYCVQQLKEF+CK
Sbjct: 472 YVSRHKATQKSIYITGESKEQVANSATVERVRKRGFEVYHTFEPIDEYCVQQLKEFGK 511
Query: 541 TLVSVTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 600
      +LVSVT NLCK+MK+IL+KXVERV +SNRLV+SPCCI
Sbjct: 532 SLVSVTKRGLPEDEEEKKQMEESKAKFENLCKLMKEITLKKKVERVTISNRLVSSPCCI 591
Query: 601 VTSTYGTAMMERIMKAQALRDNSTMGYMAKQKLEINPDHSIITLROKAEADKNDKV 660
      VTSTYGTAMMERIMKAQALRDNSTMGYMAKQKLEINPDH I+ETLROKAEADKNDKV
Sbjct: 592 VTSTYGTAMMERIMKAQALRDNSTMGYMAKQKLEINPDHPIVETLROKAEADKNDKV 651
Query: 661 KDLVILLIETALLSSGFSLEDPQTHANRIYRMINKLGLGIDEEDPTVDTSAAVTEEMPL 720
      KDLV+LL+ETALLSSGFSLEDPQTH+NAIYRMINKLGLGIDEED+ T++SAAV +E+PPL
Sbjct: 652 KDLVILLIETALLSSGFSLEDPQTHSNRIYRMINKLGLGIDEEDVTAEPSSAAVDPDEIPL 711
Query: 721 EGDDETSRMEEVD 733
      EGD+O SRMEVD
Sbjct: 712 EGDDETSRMEEVD 724

```

CPU time: 0.17 user secs. 0.01 sys. secs 0.18 total secs.

Lambda	K	H
0.316	0.134	0.372

Gapped Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 5349
 Number of Sequences: 0
 Number of extensions: 184
 Number of successful extensions: 3
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1
 length of query: 733
 length of database: 405,742,523
 effective HSP length: 134
 effective length of query: 599
 effective length of database: 405,742,389
 effective search space: 243039691011
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 T: 9
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 X3: 129 (49.7 bits)
 S1: 41 (21.6 bits)
 S2: 78 (34.7 bits)